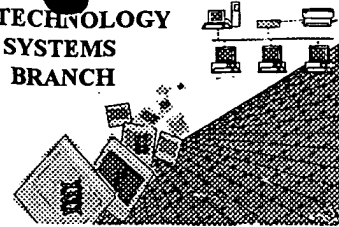


S. J. Umer

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/328,877C
Source: 1600
Date Processed by STIC: 11-18-03

RECEIVED

NOV 24 2003

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT

MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

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Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTION

SERIAL NUMBER:

09/328, 877C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ___ Wrapped Nucleic
 ___ Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ___ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ___ Misaligned Amino
 ___ Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ___ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ___ Variable Length Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ___ PatentIn 2.0
 ___ "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ___ Skipped Sequences
 ___ (OLD RULES) Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ___ Skipped Sequences
 ___ (NEW RULES) Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 ___ (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ___ Invalid <213>
 ___ Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ___ Use of <220> Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ___ PatentIn 2.0
 ___ "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ___ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



1600

Does Not Comply
Corrected Diskette Needed
SEE Additional pages @ back

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/328,877C

DATE: 11/18/2003
TIME: 13:18:14

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TECH CENTER 1600/2900

Input Set : A:\6142 revised.seq.txt
Output Set: N:\CRF4\11182003\I328877C.raw

3 <110> APPLICANT: Gurney, Mark E.
5 Li, Jinhe
7 Pauley, Adele M.
9 Pharmacia & Upjohn Company
13 <120> TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
15 Encode Them
19 <130> FILE REFERENCE: 6142
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/328,877C
C--> 25 <141> CURRENT FILING DATE: 1999-06-09
E--> 29 <160> NUMBER OF SEQ ID NOS: 27
33 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

3603 <210> SEQ ID NO: 32
3605 <211> LENGTH: 23
3607 <212> TYPE: DNA
3609 <213> ORGANISM: Artificial Sequence
3613 <220> FEATURE:
3615 <223> OTHER INFORMATION: Description of Artificial Sequence:
3617 Oligonucleotide primer
3621 <400> SEQUENCE: 32
3623 ctccagacagggtcaggacatttgg 23
E--> 3645 54

Number of sequences in
Sequence Listing is 32 not
27 given in <160>.

Remove extra material at the end
of file.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/328,877C

DATE: 11/18/2003
TIME: 13:18:15

Input Set : A:\6142_revised.seq.txt
Output Set: N:\CRF4\11182003\I328877C.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,3,5,7,9,11,13,15,17,19,21,23,25,27,29,31,33,35,37,39,41
Seq#:1; Line(s) 57,59,61,63,65,67,69,71,73,75,77,79,81,83,85,87,89,91,93,95
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Seq#:1; Line(s) 127,129,131,133,135,137,139,141,143,145,147,149,151,153,155
Seq#:1; Line(s) 157,159,161,163,165,167,169,171,173,175,177,179,181,183
Seq#:2; Line(s) 185,187,203,205,207,209,211,213,215,217,219,221,223,225,227
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: **US/09/328,877C**

DATE: 11/18/2003
TIME: 13:18:15

Input Set : A:\6142_revised.seq.txt
Output Set: N:\CRF4\11182003\I328877C.raw

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VERIFICATION SUMMARY

DATE: 11/18/2003

PATENT APPLICATION: US/09/328,877C

TIME: 13:18:15

Input Set : A:\6142_revised.seq.txt

Output Set: N:\CRF4\11182003\I328877C.raw

L:23 M:270 C: Current Application Number differs, Replaced Current Application Number
L:25 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:143 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2460
M:341 Repeated in SeqNo=1
L:289 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:2
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:2460
M:341 Repeated in SeqNo=2
L:3645 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:29 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (27) Counted (32)

<210> 1

<211> 3550

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2485)

Numeric Identifier <223> is mandatory
for 'n' and Xaa. SEE ITEM # 9 on

<220>

<221> unsure

<222> (3372)

ERROR Summary sheet,

<400> 1

<210> 2

<211> 3571

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2506)

See additional page 1.

<220>

<221> unsure

<222> (3393)

<400> 2